



SEQUENCE LISTING

<110> Nippon Institute for Biological Science

<120> novel plasmid vector

<130> PCTF0001-0

<140> 09/762,568

<141> 2001-02-06

<150> JP, Japanese Patent

<151> 1999-06-04

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 3' region of U3 and VspI restriction enzyme site to multiply RSV LTR.

<400> 1

ggcattaatg tagtcttatg caatactcct g

31

<210> 2

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 5' non coding region of p19 gene, HincII, EcoRV and BglII restriction enzyme site to multiply RSV LTR and down stream region of LTR.

<400> 2

gttaacgata tcagatctgc ttgatccacc gggcgaccag

40

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including 5' region of RSV integrase gene and BamHI restriction enzyme site to multiply RSV integrase gene.

<400> 3
 ttggtccat gcccttgaga gaggctaaag atcttc 36

<210> 4
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including 3' region of RSV
 integrase gene, polyA signal to multiply RSV
 integrase gene.

<400> 4
 tttattttaa ctctcgttgg cagcaagggt gtc 33

<210> 5
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including 5' region of U5 and
 VspI restriction enzyme site to multiply RSV LTR.

<400> 5
 ggcattaatg aagccttctg cttcattca 29

<210> 6
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including 3' region of RSV
 integrase gene, polyA signal, nuclear localization
 signal of SV40 large T antigen to multiply RSV
 integrase gene.

<400> 6
 tttattttaa accttcctct tcttcttagg actctcgttg gcagcaagg t 51

<210> 7
 <211> 858
 <212> DNA
 <213> Rous sarcoma virus

<220>
 <221> TATA_signal
 <222> (84)...(90)

<221> polyA_signal
 <222> (107)...(112)

<221> TATA_signal
 <222> (431)...(437)

<221> polyA_signal
 <222> (454)...(459)
 <223> A part of circular form of RSV DNA, tandem repeat
 LTRs and adjacent non coding region.

<400> 7

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acgatcgtgc cttattagga aggcaacaga cgggtctaac acggattgga cgaaccactg 60
aattccgcat tgcggagata ttgtatttaa gtgcctagct cgatacaata aacgccattt 120
taccattcac cacattgggtg tgcacctggg ttgatggctg gaccgttgat tccctgacga 180
ctacgagcac atgcatgaag cagaaggctt cattaatgta gtcttatgca atactcctgt 240
agtcttgcaa catgcttatg taacgatgag ttagcaacat gccttacaag gagagaaaag 300
gcaccgtgca cgacgattgg tggaaagtaag gtgggtatgat cgtagggtacg atcgtgcctt 360
attaggaagg caacagacgg gtctaacacg gattggacga accactgaat tccgcattgc 420
ggagatattg tatttaagtg cctagctcga tacaataaac gccattttac cattcaccac 480
attggtgtgc acctgggttg atggctggac cgttgattcc ctgacgacta cgagcacatg 540
catgaagcag aaggcttcat ttggtgacct cgacgtgacg gttagggaat agtggtcggc 600
cacagacggc gtggcgatcc tgccctcatc cgtctcgctt attcggggag cggacgatga 660
ccctagtaga gggggctgcg gcttaggagg gcagaagctg agtggcgctc gagggagctc 720
tactgcaggg agcccagata ccctaccgag aactcagaga gtcgttggaa gacgggaaga 780
aagcccgcag actgagcggg ccaccccagg cgtgattccg gttgctctgc gtgaccctgg 840
tcgcccgggt gatcaagc                                     858
```

<210> 8

<211> 972

<212> DNA

<213> Rous sarcoma virus

<220>

<221> CDS

<222> (1)...(972)

<223> precursor integrase or p36 protein

<221> CDS

<222> (1)...(858)

<223> mature integrase or p32 protein

<400> 8

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ccc ttg aga gag gct aaa gat ctt cat acc gct ctc cat att gga ccc 48
Pro Leu Arg Glu Ala Lys Asp Leu His Thr Ala Leu His Ile Gly Pro
1 5 10 15

cgc gcg cta tcc aaa gcg tgt aat ata tct atg cag cag gct agg gag 96
Arg Ala Leu Ser Lys Ala Cys Asn Ile Ser Met Gln Gln Ala Arg Glu
20 25 30

gtt gtt cag acc tgc ccg cat tgt aat tca gcc cct gcg ttg gag gcc 144
Val Val Gln Thr Cys Pro His Cys Asn Ser Ala Pro Ala Leu Glu Ala
35 40 45

gga gta aac cct agg ggt ttg gga ccc cta cag ata tgg cag aca gac 192
Gly Val Asn Pro Arg Gly Leu Gly Pro Leu Gln Ile Trp Gln Thr Asp
50 55 60

ttt acg ctt gag cct aga atg gcc ccc cgt tcc tgg ctc gct gtt act 240
Phe Thr Leu Glu Pro Arg Met Ala Pro Arg Ser Trp Leu Ala Val Thr
65 70 75 80
```

gtg gac acc gcc tca tca gcg ata gtc gta act cag cat ggc cgt gtc	288
Val Asp Thr Ala Ser Ser Ala Ile Val Val Thr Gln His Gly Arg Val	
85 90 95	
aca tcg gtt gct gta caa cat cat tgg gcc acg gct atc gcc gtt ttg	336
Thr Ser Val Ala Val Gln His His Trp Ala Thr Ala Ile Ala Val Leu	
100 105 110	
gga aga cca aag gcc ata aaa aca gat aac ggg tcc tgc ttc acg tct	384
Gly Arg Pro Lys Ala Ile Lys Thr Asp Asn Gly Ser Cys Phe Thr Ser	
115 120 125	
aaa tcc acg cga gag tgg ctc gcg aga tgg ggg ata gca cac acc acc	432
Lys Ser Thr Arg Glu Trp Leu Ala Arg Trp Gly Ile Ala His Thr Thr	
130 135 140	
ggg att ccg ggt aat tcc cag ggt caa gct atg gta gag cgg gcc aac	480
Gly Ile Pro Gly Asn Ser Gln Gly Gln Ala Met Val Glu Arg Ala Asn	
145 150 155 160	
cgg ctc ctg aaa gat agg atc cgt gtg ctt gcg gag ggg gac ggc ttt	528
Arg Leu Leu Lys Asp Arg Ile Arg Val Leu Ala Glu Gly Asp Gly Phe	
165 170 175	
atg aaa aga atc ccc acc agc aaa cag ggg gaa cta tta gcc aag gca	576
Met Lys Arg Ile Pro Thr Ser Lys Gln Gly Glu Leu Leu Ala Lys Ala	
180 185 190	
atg tat gcc ctc aat cac ttt gag cgt ggt gaa aac acg aaa aca ccg	624
Met Tyr Ala Leu Asn His Phe Glu Arg Gly Glu Asn Thr Lys Thr Pro	
195 200 205	
ata caa aaa cac tgg aga cct acc gtt ctt aca gaa gga ccc ccg gtt	672
Ile Gln Lys His Trp Arg Pro Thr Val Leu Thr Glu Gly Pro Pro Val	
210 215 220	
aaa ata cga ata gag aca ggg gag tgg gaa aaa gga tgg aac gtg ctg	720
Lys Ile Arg Ile Glu Thr Gly Glu Trp Glu Lys Gly Trp Asn Val Leu	
225 230 235 240	
gtc tgg gga cga ggt tat gcc gct gtg aaa aac agg gac act gat aag	768
Val Trp Gly Arg Gly Tyr Ala Ala Val Lys Asn Arg Asp Thr Asp Lys	
245 250 255	
gtt att tgg gta ccc tct cga aaa gtt aaa ccg gac atc acc caa aag	816
Val Ile Trp Val Pro Ser Arg Lys Val Lys Pro Asp Ile Thr Gln Lys	
260 265 270	
gat gag gtg act aag aaa gat gag gcg agc cct ctt ttt gca ggc att	864
Asp Glu Val Thr Lys Lys Asp Glu Ala Ser Pro Leu Phe Ala Gly Ile	
275 280 285	
tct gac tgg ata ccc tgg gga gac aag caa gaa gga ctc caa gga gaa	912
Ser Asp Trp Ile Pro Trp Gly Asp Lys Gln Glu Gly Leu Gln Gly Glu	
290 295 300	

acc gct agc aac aag caa gaa aga ccc gga gaa gac acc ctt gct gcc 960
 Thr Ala Ser Asn Lys Gln Glu Arg Pro Gly Glu Asp Thr Leu Ala Ala
 305 310 315 320

aac gag agt taa 972
 Asn Glu Ser *

<210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including 5' region of GFP
 gene and a part of NheI restriction enzyme site to
 multiply GFP gene.

<400> 9
 ctagcgctac cggtcgccac c 21

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including antisense sequence
 of GFP ORF to multiply a part of GFP gene.

<400> 10
 gttgccgtcc tccttgaagt 20

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including U5 region LTR
 sequence to
 multiply a part of integrated plasmid vector.

<400> 11
 ttggtgtgca cctgggttga t 21

<210> 12
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed PCR primer including 5' end of GFP ORF
 sequence to multiply a part of GFP gene.

<400> 12

atggtgagca agggcgagga gctgttcacc ggggtg

36

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed PCR primer including a part of GFP ORF
sequence to multiply a part of GFP gene.

<400> 13

gtcgagctgg acggcgacgt

20